

Dr. Vladimir B. Teif

ADDRESS:

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Web site: <http://generegulation.org>

ACADEMIC QUALIFICATIONS:

- 2017: Fellow of the Higher Education Academy, UK (FHEA)
2004: PhD, *summa cum laude*
Service de Biochimie et Génétique Moléculaire, CEA/Saclay, French Commission for Atomic Energy, INTAS Fellow (http://cordis.europa.eu/programme/rcn/493_en.html), joint program with the Belarus National Academy of Sciences.
Supervisors: Dr. Jean-Louis Sikorav and Prof. Dmitry Lando
2000: MSc (Diploma), *honors*, Belarus State University, Minsk

PROFESSIONAL APPOINTMENTS:

- 2015 – current: University of Essex, UK. *Lecturer* (with permanency)
Since 2019 also serve as *Academic Offences Officer* for the School of Life Sciences.
2008 – 2015: German Cancer Research Center (DKFZ) and BioQuant, Heidelberg, Germany
2011 – 2015: BIOMS Postdoctoral Fellowship (www.bioms.de)
2009 – 2011: Fellow of the Cellnetworks Cluster of Excellence (www.cellnetworks.de)
2008 – 2009: DKFZ Guest Scientist (www.dkfz.de), Group of Prof. Karsten Rippe.
2004 – 2008: Belarus National Academy of Sciences, Institute of Bioorganic Chemistry, Minsk
2009 – 2010: Senior Scientist (affiliated, while already working full-time in Germany).
2004 – 2008: Research Scientist (affiliated, while working 50% in Israel, USA & France).

VISITING SCIENTIST POSITIONS:

- 02/2008 – 06/2008: University of California San Diego, Centre of Theoretical Biological Physics (CTBP Visiting Scientist Fellowship, working in the group of Prof. Terry Hwa).
03/2008: Institute of Complex Systems, Santa Fe, NM, USA
09/2007: International Center of Theoretical Physics, Trieste, Italy (UNESCO Fellow)
04/2007 – 05/2007, 11/2005 – 02/2006: Hebrew University, Jerusalem
(FEBS Fellowship, groups of Prof. Avinoam Ben-Shaul and Dr. Daniel Harries)

RESEARCH GRANTS

- 1) Wellcome Trust Seed Award, 2016-2018. "Nucleosome repositioning as a mechanism for cell memory in cancer transitions", **PI. £85,432.**
- 2) @RAction grant, ANR (France), 2015. "Deciphering and modifying epigenetic mechanisms of stem cell development", **PI. €870,000.** (Awarded, but not taken due to relocation to the UK).
- 3) Merck grant "Chaire Junior Fondagen", 2015, **PI. €275,000** (awarded to complement a Group Leader offer in iSSB, Evry, France, but the award was not taken due to relocation to the UK).
- 4) Sonata-BIS-4 grant, NCN (Poland), 2015, "Predicting differential transcription factor binding in chromatin", **PI. €500,000.** (Awarded, but not taken due to relocation to the UK).
- 5) Intramural Grant of the German Cancer Research Center, 2012-2014, "Calculating transcription factor binding maps in chromatin", **PI. €120,000**
- 6) Intramural Grant of the German Cancer Research Center, 2012-2013, "Developing a software suite for the analysis of epigenetic regulation from high-throughput sequencing data", **Co-PI** with Dr Yevhen Vainshtein. **€20,000**

- 7) Belarus National Foundation of Fundamental Research, Grant #B10M-060, "Investigation of chromatin rearrangements in tumor and normal tissues", 2010, **PI, €10,000**
- 8) Belarusian Governmental Program "Bio-rational Pesticides-II", "Study of synergistic effects of pesticide combinations using statistical analysis", 2009, **co-PI** with Prof Lando. **€10,000**
- 9) Belarus National Foundation of Fundamental Research, Grant #B06M-127 "Biomolecular interactions with condensed DNA", 2006-2008, **PI. €10,000**
- 10) Belarus National Foundation of Fundamental Research, #B02M-091 "Influence of anticancer and carcinogenic metal complexes on DNA condensation", 2002-2004, **PI. €10,000**

OUTREACH, NETWORKING AND TEACHING GRANTS

- 11) Two grants of the Global Challenges Research Fund (GCRF) (**£2,616** and **£1,750**) to establish collaboration with Prof Ranjith Padinhateeri (Indian Institute of Technology Bombay) and to organise a workshop "Biophysics of Chromatin", July 8, 2019, Colchester, UK.
- 12) The Royal Society Partnership Grant, 2018, **Co-PI** with Dr Mari Chikvaidze, **£3,000**.
- 13) LabArchives Development Grant, 2017-2021, **PI. \$6,200**.
- 14) Proficio Grant to develop a PhD level course on NGS analysis, 2016, **PI, £1,200**.

HONORS

- 2018: Publons award for top peer-reviewers (top 1% reviewers in Biology & Biochemistry)
- 2011: BIOMS Fellowship, DKFZ and BioQuant, Germany, 2011-2015
- 2009: German Excellence Cluster Cellnetworks Fellowship, BioQuant, Germany, 2009-2010
- 2009: DKFZ Guest Scientist Grant, DKFZ and BioQuant, Germany, 2008-2009
- 2008: CTBP Visiting Scientist Grant, University of California at San Diego, USA, 02-06/2008
- 2008: SFI Visiting Scientist Grant, Institute of Complex Systems, Santa Fe, USA, 04/2008
- 2007: Boehringer Ingelheim Short-Term Fellowship, DKFZ, Germany 10/2007
- 2007: UNESCO Visiting Scientist, International Center of Theoretical Physics, Trieste, 09/2007
- 2007: President's Fellowship (top 100 young scientists of Belarus)
- 2007: FEBS Short-Term Fellowship, Hebrew University, Jerusalem, Israel
- 2006: Golda Meir Fellowship, Hebrew University, Jerusalem (not taken for family reasons)
- 2004: Fellow of the Belarus National Academy of Sciences, 2004
- 2002: INTAS Young Scientist Ph.D. Fellowship, CEA/Saclay, France, 2002-2004
- 2000-2016: 14 Young Scientist Travel Awards (see page 7); 1 best student poster award.

PROFESSIONAL SERVICE

Member of the Management Committee for the European COST action "International Nucleome Consortium" <https://e-services.cost.eu/action/CA18127>

Conference Organiser:

- "Biophysics of Chromatin", University of Essex, UK. 08/07/2019
- "Chromatin and Epigenomics", University of Essex, UK. 14/09/2017; 13/09/2019.

Conference session chair:

Biomolecular Structure and Dynamics, Albany 2015, the 19th Conversation, the State University of New York, Albany, NY, USA, June 9-13, 2015.

Associate Editor for *AIMS Biophysics* (since 2014). Also edited the special issue "Chromatin and Epigenetics" <http://www.aimspress.com/newsinfo/133.html>

Associate Editor for *biOverlay* (2018); **Editor** for *Frontiers in Genetics* (since 2013);

Reviewed grants for BBSRC, CRUK, Breast Cancer NOW and Daphne Jackson (UK), ANR (France), DFG (Germany), ISF (Israel), NSERC (Canada), NWO (Netherlands), PNF (Poland).

Reviewed for > 40 journals including *Cell*, *NAR*, *PNAS*, *Genome Research*, *PLoS Comput. Biol.*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Biology*, *BMC Genomics*, *Briefings in Bioinformatics*, *Biophysical Journal*, etc. See <https://publons.com/author/1308717/vladimir-teif>

External PhD examiner for Dr Joanna Mitchelmore, University of Cambridge, 2018

STEM Ambassador: scientific outreach activities for the Claremont High School Academy.

PUBLICATIONS

*Asterisk indicates the corresponding author. Last updated: September 30, 2019

1. Clarkson C.T., Deeks E.A., Samarista R., Mamayusupova H., Zhurkin V.B., **Teif V.B.*** (2019) CTCF-dependent chromatin boundaries formed by asymmetric nucleosome arrays with decreased linker length. *Nucleic Acids Res.* (accepted, in press)
2. Antwi E.B., Olins A., Teif V.B., Bieg M., Bauer T., Gu Z., Brors B., Eils R., Olins D., Ishaque N. (2019) Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. *bioRxiv preprint*. Under review
3. Wiehle L., Thorn G.J., Raddatz G., Clarkson C.T., Rippe K., Lyko F., Breiling A. *, **Teif V.B.*** (2019) DNA (de)methylation in embryonic stem cells controls CTCF-dependent chromatin boundaries. *Genome Research* **29**, 750-761. [Featured on the journal cover](#).
4. Mallm J.-P., Iskar M., Ishaque N., Klett L.C., Kugler S.J., Muino J.M., **Teif V.B.**, Poos A.M., Großmann S., Erdel F., Tavernari D., Koser S.D., Schumacher S., Brors B., König R., Remondini D., Vingron M., Stilgenbauer S., Lichter P., Zapatka M., Mertens D., Rippe K. (2019) Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. *Mol Syst Biol* **15**, e8339. [Featured on the journal cover](#).
5. **Teif V.B.*** and Clarkson C.T. (2019) Nucleosome Positioning. In: Guenther, R. and Steel, D. (eds.), *Encyclopedia of Bioinformatics and Computational Biology*, vol. 2, pp. 308–317. Oxford: Elsevier.
6. Pavlaki I., Docquier F., Chernukhin I., Kita G., Gretton S., Clarkson C.T., ***Teif V.B.**, ***Klenova E.** (2018) Poly(ADP-ribosyl)ation dependent changes in CTCF-chromatin binding and gene expression in breast cells. *Biochim Biophys Acta (BBA) – Gene Regulatory Mechanisms* **1861**, 718-730.
7. Vainshtein Y., Rippe K. and **Teif V.B.*** (2017). NucTools: analysis of chromatin feature occupancy profiles from high-throughput sequencing data. *BMC Genomics* **18**, 158.
8. **Teif V.B.***, Mallm J.-P., Sharma T., Mark Welch D.B., Rippe K., Eils R., Langowski J., Olins A.L. and Olins D.E.* (2017). Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. *Nucleus* **8**, 188-204.
9. **Teif V.B.*** (2016) Nucleosome positioning: resources and tools online. *Briefings in Bioinformatics* **17**, 745-757.
10. **Teif V.B.*** and Cherstvy A.G. (2016). Chromatin and epigenetics: current biophysical views. *AIMS Biophysics* **3**, 88-98.
11. **Teif V.B.***, Kepper N., Yserentant K., Wedemann G., Rippe K. (2015). Affinity, stoichiometry and cooperativity of heterochromatin protein 1 (HP1) binding to nucleosomal arrays. *J. Phys.: Condens. Matter.* **27**, 064110
12. Salih B.*, **Teif V.B.**, Tripathi V., Trifonov E.N. (2015) Strong nucleosomes of mouse genome in recovered centromeric sequences. *J. Biomol. Struct. & Dynam.* **33**, 1164-75.
13. **Teif V.B.***, Beshnova D.A., Marth C., Vainshtein Y., Mallm J.-P., Höfer T. and Rippe K.* (2014). Nucleosome repositioning links DNA (de)methylation and differential CTCF binding during stem cell development. *Genome Research.* **24**, 1285-1295

14. Beshnova D.A., Cherstvy A.G. Vainshtein Y. and **Teif V.B.*** (2014). Regulation of the nucleosome repeat length *in vivo* by the DNA sequence, protein concentrations and long-range interactions. *PLoS Comput. Biol.* **10**(7):e1003698.
15. Cherstvy A.G.* and **Teif V.B.** (2014). Electrostatic effect of H1 histone binding on the nucleosome repeat length. *Phys. Biol.* **11**, 044001.
16. **Teif V.B.*** (2014). On the Sociology of Science 2.0. In "Opening Science: the evolving guide on how the Internet is changing research, collaboration and scholarly publishing", Eds. S. Bartling, S. Friesike. Springer, 2014, IX, 335 p. 43 illus. | ISBN 978-3-319-00026-8.
17. Schöpflin R., **Teif V.B.**, Müller O., Weinberg C., Rippe K., Wedemann G.* (2013). Modeling nucleosome distributions from experimental nucleosome positioning maps of cell ensembles. *Bioinformatics.* **29**, 2380-2386.
18. Cherstvy A.G.* and **Teif V.B.** (2013) Structure-driven homology pairing of chromatin fibers: The role of electrostatics and protein bridging. *J. Biol. Phys.* **39**, 363-385.
19. **Teif V.B.***, Erdel F., Beshnova D.A., Vainshtein Y., Mallm J.-P., Rippe K. (2013) Taking into account nucleosomes for predicting gene expression. *Methods* **62**, 26-38.
20. **Teif V.B.*** (2013). Science 3.0: Corrections to the Science 2.0 paradigm. ArXiv:1301.2522.
21. **Teif V.B.***, Vainshtein Y., Caudron-Herger M., Mallm J.-P., Marth C., Höfer T., *Rippe K. (2012) Genome-wide nucleosome positioning during embryonic stem cell development. *Nature Struct. Mol. Biol.* **19**, 1185-92.
22. **Teif V.B.*** and Rippe K. (2012) Calculating transcription factor binding maps for chromatin. *Briefings in Bioinformatics* **13**, 187-201.
23. **Teif V.B.***, Shkrabkou A.V., Egorova V.P., Krot V.I. (2012) Nucleosomes in gene regulation: theoretical approaches. *Molecular Biology* **46**, 1-10.
24. **Teif V. B.*** and Bohinc K. (2011). Condensed DNA: condensing the concepts. *Progress in Biophysics and Molecular Biology* **105**, 208-222.
25. **Teif V.B.*** and Rippe K.* (2011) Nucleosome mediated crosstalk between transcription factors at eukaryotic enhancers. *Physical Biology* **8**, 044001.
26. Längst G.*, **Teif V.B.** and Rippe K.* (2011). Chromatin remodeling by translocation of nucleosomes. In "Genome organization and function in the cell nucleus", Ed. K. Rippe, Wiley-VCH, Weinheim. P. 111-139.
27. **Teif V. B.*** (2010). Predicting gene-regulation functions: Lessons from temperate bacteriophages. *Biophys. J.* **98**, 1247-1256.
28. **Teif V.B.***, Ettig R. and Rippe K.* (2010). A lattice model for transcription factor access to nucleosomal DNA. *Biophys. J.* **99**, 2597-2607.
29. **Teif V.B.*** and Rippe K.* (2010). Statistical-mechanical lattice models for protein-DNA binding in chromatin. *J. Phys.: Condens. Matter.* **22**, 414105.
30. **Teif V. B.***, Harries D., Lando D.Y. and Ben-Shaul A. (2010). Matrix formalism for sequence-specific polymer binding to multicomponent lipid membranes. In "Membrane-active peptides: methods and results on structure and function", Ed. M. Castanho, International University Line, La Jolla. P. 29-52.
31. **Teif V. B.*** and Rippe K.* (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. *Nucleic Acids Res.* **37**, 5641-5655.
32. **Teif V. B.***, Harries D., Lando D. Y. and Ben-Shaul A. (2008). Matrix formalism for site-specific binding of unstructured proteins to multicomponent lipid membranes. *J. Pept. Sci.* **14**, 368-373.
33. **Teif V. B.*** (2007). General transfer matrix formalism to calculate DNA-protein-drug binding in gene regulation: Application to O_R operator of phage λ . *Nucleic Acids Res.* **35**, e80.

34. **Teif V. B.*** (2005). Ligand-induced DNA condensation: choosing the model. *Biophys. J.* **89**, 2574-2587.
35. **Teif V. B.** and Lando D. Y.* (2003). DNA condensation caused by ligand binding. In "Bioregulators: investigation and application", Ed. F.A. Lakhvich, Technoprint, Minsk, P. 116-128.
36. Lando D. Y.* and **Teif V. B.** (2002). Modeling of DNA condensation and decondensation caused by ligand binding. *J. Biomol. Struct. Dynam.* **20**, 215-222.
37. **Teif V. B.**, Haroutunian S. H., Vorob'ev V. I. and Lando D. Y.* (2002). Short-range interactions and size of ligands bound to DNA strongly influence adsorptive phase transition caused by long-range interactions. *J. Biomol. Struct. Dynam.* **19**, 1103-1110.
38. **Teif V. B.** and Lando D. Y.* (2001). Calculation of DNA condensation caused by ligand adsorption. *Molecular Biology* **35**, 117-119.
39. **Teif V. B.***, Lando D. Y. (2001). DNA condensation caused by ligand binding may serve as a sensor. In "Sensor Technology 2001", ed. M. Elwenspoek, Kluwer, Dordrecht, P. 155-160.
40. Lando D. Y.* and **Teif V. B.** (2000). Long-range interactions between ligands bound to a DNA molecule give rise to adsorption with the character of phase transition of the first kind. *J. Biomol. Struct. Dynam.* **17**, 903-911.

INVITED TALKS

1. Microdomain formation in chromatin, Biophysics of Epigenetics and Chromatin Workshop, Edinburgh, April 16-17, 2018.
2. Interplay of epigenetic modifications, TF binding and nucleosome positioning, CECAM-Lorentz Workshop "Multiscale-modelling of nucleosomes and their positioning on DNA", January 15-19, 2018, Lausanne.
3. Microdomain formation in chromatin, Multiscale Modeling and Experimental Approaches to Genome Organization, April 2-7, 2017, Ecole de Physique, Les Houches, France.
4. Predicting differential transcription factor binding in cell transformations, Collège de France, Paris, November 2, 2015
5. Predicting differential transcription factor binding in cell transformations, University of Strasbourg, France, 25 September, 2015.
6. Predicting differential transcription factor binding in cell transformations, CNRS, Paris, April 1, 2015.
7. Predicting differential transcription factor binding in cell transformations, University of Würzburg, Germany, 13 January 2015.
8. Predicting differential transcription factor binding during cell transformations, University of Essex, UK, November 6, 2014.
9. Deciphering the rules of stem cell development, Centre d'Immunologie de Marseille-Luminy, University of Marseille, France, September 24, 2014.
10. Interplay of CTCF binding, DNA methylation and nucleosome positioning, Weizmann Institute of Science, Israel, September 16, 2014.
11. Interplay of CTCF binding, DNA methylation and nucleosome positioning, Hebrew University, Israel, September 14, 2014.
12. Interplay of CTCF binding, DNA methylation and nucleosome positioning, University of Haifa, Israel, September 11, 2014.
13. Deciphering epigenetic mechanisms of stem cell differentiation, University of Gdansk, Poland, 27 June 2014.
14. Deciphering epigenetic mechanisms of stem cell differentiation, Max F. Perutz Laboratories, Vienna, Austria, May 28, 2014.
15. Macromolecule assembly on the DNA, Friedrich-Alexander-Universität Erlangen-Nürnberg, Fürth, Germany, March 4, 2014.
16. Deciphering rules of epigenetic regulation using modeling and high-throughput sequencing experiments, Institute of Systems and Synthetic Biology, Evry, France, February 15, 2014.

17. Interplay between DNA methylation, nucleosome positioning and transcription factor binding during stem cell development, Max Plank Institute for Molecular Genetics, Berlin, 5th November 2013.
18. Deciphering epigenetic mechanisms of stem cell differentiation, Humboldt University, Berlin, 4th November 2013.
19. Deciphering epigenetic mechanisms of stem cell differentiation, University of Sheffield, UK, October 16, 2013.
20. Deciphering epigenetic mechanisms of stem cell differentiation, CNRS, Gif-sur-Yvette, France, October 10, 2013.
21. Deciphering epigenetic mechanisms of stem cell differentiation, BIOTEC, TU Dresden, April 29, 2013.
22. Deciphering epigenetic mechanisms of stem cell differentiation, Bar Ilan University, Israel, 24 July 2013.
23. Deciphering epigenetic mechanisms of stem cell differentiation, Ecole Normale Supérieure de Lyon, France, July 6, 2013
24. Nucleosome positioning in cell differentiation. Max-Plank-Institute for the Physics of Complex Systems, Dresden, March 20, 2012.
25. Quantitative description of gene regulation in chromatin. Institut de cancérologie Gustave Roussy, Villejuif, France, October 4, 2011.
26. Calculating transcription factor binding in chromatin. Gene Center, LMU, Munich, Germany, 18 April, 2011.
27. Deciphering epigenetic algorithms of the cell. Center of Quantitative Biology, Düsseldorf University, December 16, 2010.
28. Deciphering epigenetic algorithms of the cell. International Symposium on Biological Physics, Max-Plank-Institute for the Physics of Complex Systems and Max-Plank-Institute of Molecular Cell Biology and Genetics, Dresden, December 2-3, 2010.
29. Predicting gene-regulation functions, University College Dublin, December 3, 2009.
30. Predicting gene-regulation functions, University of Warwick, July 6, 2009.
31. Quantitative description of gene regulation. Imperial College London, May 7, 2008.
32. Lattice models for stat.-mech. description of gene regulation, Institute of Complex Systems, Santa Fe, NM, USA, March 25, 2008.
33. Lattice models for gene regulation, UCSD, San Diego, USA, February 10, 2008.
34. Lattice models for DNA-ligand binding, Hebrew University, Jerusalem, January 5, 2006.
35. DNA condensation induced by polyamines and metal ions, Engelhard Institute of Molecular Biology, Moscow, Russia, March 27, 2004.

CONTRIBUTED TALKS

36. Microdomain formation in chromatin, Quantitative Methods in Gene Regulation IV, December 18-19, 2017, Cambridge, UK.
37. Nucleosome repositioning in cancer transitions, Genome 10K and Genome Science Conference, 29 August – 1 September 2017, Norwich, UK.
38. Interplay of nucleosome positioning, covalent modifications and transcription factor binding, European Conference on Mathematical and Theoretical Biology, Nottingham, UK, 16 July, 2016.
39. Chromatin rearrangement and differential CTCF binding during cell transformations. London Chromatin Club, Kings College London, 30 June, 2016
40. Integrative analysis of combinatorial chromatin interactions using high-throughput sequencing data, 12th International Symposium on Bioinformatics Research and Applications, Minsk, Belarus, June 5-8, 2016.
41. Developing a software suite to analyze the interplay between nucleosome arrangement, DNA methylation and transcription factor binding, "The next NGS Challenge", May 14-16, 2013, Valencia, Spain. Published: Teif V.B., Beshnova D., Vainshtein Y., Höfer T., Rippe K. (2013). Developing a software suite to analyze the interplay between nucleosome arrangement, DNA methylation and transcription factor binding. *EMBnet.journal* 19A, 39-40.

42. Nucleosome re-arrangement as a feedback mechanism between DNA methylation and transcription factor binding. Joint International Meeting of the German Society for Cell Biology (DGZ) and the German Society for Developmental Biology (GfE), Heidelberg, March 20 – 23, 2013.
43. Calculating transcription factor binding maps for chromatin. International Chromosome Conference, Manchester, September 2, 2011. Chromatin remodeling during differentiation of mouse embryonic stem cells. 4th Workshop “Epigenetics at DKFZ”, DKFZ, Heidelberg, January 16, 2012.
44. Why biological logic is NOT Boolean? ERASysBio Summer School, Universidad de Verano de Adeje, Tenerife, Spain, July 29, 2010. Calculating transcription factor binding in chromatin. Summer School on Systems Biology, Kloster Seeon, Germany, 16-18 March, 2011.
45. Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. Biophysics of Chromatin Workshop, February 4-6, 2009, Heidelberg, Germany.
46. Polyamine-induced DNA condensation. International Summer School “Multiple aspects of DNA and RNA: from biophysics to bioinformatics”, Les Houches, France, 2 August – 24 August, 2004.

Presentations selected for young scientist travel awards:

1. Lando D. Y. and **Teif V. B.** Influence on double helix stability of the antibiotics, linked to DNA by flexible polymeric molecules. Third Meeting of Belarusian Society of Biophysicists and Photobiologists, Minsk, October 21-23, 1998. P. 206. **Best Student Poster Award.**
2. **Teif V. B.** and Lando D. Y. Conditions for DNA phase transition induced by ligand binding. 10th International Congress of Human Genetics, May 15-19, 2001, Vienna, Austria. Published in *Europ. J. Human Genet.* 9 suppl. 1, 241 (2001).
3. **Teif V. B.** and Lando D. Y. Modeling of DNA condensation and decondensation caused by ligand binding. “DNA in Chromatin: at the Frontiers of Biology, Biophysics and Genomics”, Arcachon, France, March 23-29, 2002. P. 189.
4. **Teif V. B.** and Lando D. Y. DNA condensation-decondensation transition caused by ligand binding. 14th World Biophysics Congress, Buenos Aires, Argentina, April 27 – May 1, 2002. P. 42.
5. **Teif V. B.**, Vorob’ev V. I. and Lando D. Y. A Single DNA chemical modification by cisplatin may cause long-range changes in protein binding to DNA. Results of computer modeling. European Human Genetics Conference 2002, Strasbourg, France, May 25 – 28, 2002. Published in *Europ. J. Human Genet.* 10 suppl. 1, 104 (2002).
6. **Teif V. B.**, Lando D. Y. On the cooperativity of metal ion binding to the bases of single-stranded DNA. 29th FEBS Congress, Warsaw, 26 June – 1 July, 2004. In *Europ. J. Biochem.* 271(1), 19 (2004).
7. Soft condensed matter physics in molecular and cell biology, Edinburgh, UK, 29 March – 8 April, 2004.
8. International Summer School “Multiple aspects of DNA and RNA: from biophysics to bioinformatics”, Les Houches, France, 2 August – 24 August, 2004.
9. **Teif V. B.** General transfer matrix formalism for protein-DNA binding. International Congress of Biochemistry and Molecular Biology, June 16-23, 2006, Kyoto, Japan. **IUBMB Award.**
10. Teif V.B., Lando D.Y., Ben-Shaul A.. A transfer matrix model for the binding of the unfolded MARCKS protein to a mixed fluid lipid membrane. 2nd Workshop on Biophysics of Membrane-Active Peptides, Lisbon, 1-4 April, 2007. **FEBS Award.**
11. **Teif V. B.** General transfer matrix formalism for protein-DNA binding. Biophysical Congress, 2008, Long Beach, USA. **Biophysical Society International Travel Award**
12. **Teif V. B.** and Rippe K. (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. Advanced Lecture Course "New Developments in Quantitative Molecular Bioscience", Spetses, 10-17 Sept. 2008. **FEBS Award.**

13. **Teif V. B.** and Rippe K. (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. International Conference "From DNA-Inspired Physics to Physics-Inspired Biology", Trieste, 1-5 June, 2009.
14. **Teif V. B.** (2016) Microdomain formation in chromatin. EMBO Conference "From Functional Genomics to Systems Biology", Heidelberg, November 12-15 2016, **EMBL Travel Grant**.

TEACHING

Current teaching (University of Essex):

BS222 Genome Science (Module supervisor)
 BS312 Genome Bioinformatics; BS320 Human Molecular Genetics
 BS349 Molecular Basis of Cancer; 3rd Year BSc Research Projects
 BS932 Advanced Cancer Biology; BS933 Practical Skills in Cancer Research
 BS984 MSc Molecular Medicine; BS986 MSc Biotechnology

Annual Ph.D. lectures and practical courses:

- "Online tools for researchers";
- "Next Generation Sequencing Analysis" (1-day practical course, director)

Teaching before coming to the University of Essex:

- "Interactions of Proteins and Nucleic Acids - Techniques and Applications", Heidelberg University, Germany, 2009-2012 (assisted Prof. Karsten Rippe).
- "Introduction to Biophysics of Nucleic Acids", Institute of Molecular and Atomic Physics, Minsk, 2000-2002 (independently developed and delivered a new course).

Supervision of PhD students and staff:

Christopher Clarkson, 2017 – current (PhD student)
Dr. Hulkar Mamayusupova, 2018 (joint with Prof Elena Klenova)
Dr. Graeme Thorn, 2017 – 2018 (funded by the Wellcome Trust Seed Award)
Dr. Svetlana Gretton, 2016 – 2017 (joint supervision with Prof Elena Klenova)
Dr. Ioanna Pavlaki, 2015 – 2016 (joint supervision with Prof Elena Klenova)
Dr. Daria Beshnova, 2012 – 2013 (joint supervision with Prof Karsten Rippe)

Supervision of MSc (taught) and MSD (research) students (University of Essex):

Varvara Koraki Folli, MSD (current)
Chelsea Fox, MSD (current)
Jonathan Lam, MSc (taught), 2019 (current)
Christopher Armstrong, MSc (taught), 2018
Navid Shafiei, MSc (taught), 2017
Joshua Burton, MSc (taught), 2016
Tanvi Sharma, MSc (taught), 2016

Supervision of undergraduate students funded by competitive fellowships:

Kristan Piroeva (Genetics Society Summer Fellowship, 2019);
Emma Deeks and Varvara Koraki Folli (Frontrunner Plus Fellowships, 2018/19);
Ralph Samarista (Wellcome Trust Vacation Fellowship, 2018).